

## SEQUENCE LISTING

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Lewis, Norman G

<120> Recombinant Secoisolariciresinol Dehydrogenase, and  
methods of Use

<130> wsur113787

<140> Not yet assigned

<141> 1999-04-23

<150> 60/082,977

<151> 1998-04-24

<160> 25

<170> PatentIn Ver. 2.0

<210> 1

<211> 819

<212> DNA

<213> Forsythia x intermedia

<220>

<221> CDS

<222> (1)..(819)

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ctt ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc	96
Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu	
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ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa	144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu	
35 40 45	
tta ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac	192
Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr	
50 55 60	
atc cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac	240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp	
65 70 75 80	
aac aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca	288
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala	
85 90 95	
gga att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca	336
Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala	
100 105 110	

100	105	110	
gac ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc			384
Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys			
115	120	125	
atg aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata			432
Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile			
130	135	140	
att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat			480
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His			
145	150	155	160
gcc tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg			528
Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu			
165	170		175
gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct			576
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro			
180	185		190
ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat			624
Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn			
195	200		205
gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt			672
Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly			
210	215		220
cca aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct			720
Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala			
225	230	235	240
agt gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga			768
Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly			
245	250		255
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Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp			
260	265		270
tct			819
Ser			

&lt;210&gt; 2

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Forsythia x intermedia

&lt;400&gt; 2

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 Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr  
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 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp  
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 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala  
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 Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala  
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 Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys  
                   115                                  120                                  125  
 Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile  
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 Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu  
                                   165                                  170                                  175  
 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro  
                   180                                  185                                  190  
 Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn  
                   195                                  200                                  205  
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 Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala  
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 Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly  
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 Ser

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gga aaa gtt gcc ctt ata aca gga gga gcc agt gga att gga gaa acc 96  
 Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr  
 20 25 30

aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat 144  
 Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp  
 35 40 45

gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc act tcc 192  
 Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser  
 50 55 60

aat tcc acc tac atc cac tgt gat gtt act aat gaa gac ggt gtt aaa 240  
 Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys  
 65 70 75 80

aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg 288  
 Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met  
 85 90 95

ttc agc aat gca gga att tct gat ccc aac agg ccc cgc atc ata gac 336  
 Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp  
 100 105 110

aac gaa aaa gca gac ttt gaa cgc gtt ttc agt gta aat gta acc gga 384  
 Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly  
 115 120 125

gtt ttc cta tgc atg aag cac gca gca cgt gtt atg att cca gca cgc 432  
 Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg  
 130 135 140

agt ggc aac ata att tcc act gct agt tta agc tca act atg ggt ggt 480  
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 145 150 155 160

ggt tct tca cat gcc tat tgt ggt tca aag cat gct gtg tta ggc ctt 528  
 Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu  
 165 170 175

act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat 576  
 Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn  
 180 185 190

tgt ttg tct cct ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca 624  
 Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser  
 195 200 205

ggg att aaa aat gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga 672  
 Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly  
 210 215 220

aat ctg aaa ggt cca aaa ttt aat gtt gag gat gtt gcc aat gca gct 720

Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala  
 225 230 235 240  
 ctt tat ctg gct agt gat gag gca aaa tac gtg agt gga cac aat ctg 768  
 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu  
 245 250 255  
 ttc att gat gga ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc 816  
 Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe  
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 35 40 45  
 Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser  
 50 55 60  
 Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys  
 65 70 75 80  
 Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met  
 85 90 95  
 Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp  
 100 105 110  
 Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly  
 115 120 125  
 Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg  
 130 135 140  
 Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly  
 145 150 155 160  
 Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu  
 165 170 175  
 Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn  
 180 185 190

Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser  
 195 200 205  
 Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly  
 210 215 220  
 Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala  
 225 230 235 240  
 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu  
 245 250 255  
 Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe  
 260 265 270  
 Gln Tyr Pro Asp Ser  
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 Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu  
 20 25 30  
 ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa 144  
 Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu  
 35 40 45  
 tta ggt cac tca gtt gtc gag gcc att ggc cct tcc aat tcc acc tac 192  
 Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr  
 50 55 60  
 atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac 240  
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp  
 65 70 75 80  
 aac aca gtt tca acc tat gga aaa ctg gac att atg ttc aac aat gca 288  
 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala  
 85 90 95  
 gga att tct gat ccc tac aag ccc cgg gtc ata gac aac gaa aaa gca 336  
 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala  
 100 105 110  
 gac ttt gaa cgc gtt ctc agt gtn aat gtn acc gga gtt ttc cta ttt 384

Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe  
 115 120 125  
 atg aag cac gca gca cgc att atg gtt cca gca cga aat ggc tgc ata 432  
 Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile  
 130 135 140  
 att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat 480  
 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His  
 145 150 155 160  
 gct tat tgt ggt gca aaa cat gct gta tta ggc ctt act agg aat ctg 528  
 Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu  
 165 170 175  
 gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct 576  
 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro  
 180 185 190  
 ttc ggg ctt cct acg cct cta gcc aag aaa ttt tca ggg att gaa aat 624  
 Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn  
 195 200 205  
 gat gta gac ttt gcg aat gca ata gaa cat gcg gga aat ctg aaa ggt 672  
 Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly  
 210 215 220  
 aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt ttt ctg gct 720  
 Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala  
 225 230 235 240  
 agt gat gag gca caa tat gtg agt gga caa aat ctg ttc atc gat gga 768  
 Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly  
 245 250 255  
 ggg ttc agc gtc tgc aat tct gca atc aaa atg ttc caa tat cca gac 816  
 Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp  
 260 265 270  
 tct 819  
 Ser

&lt;210&gt; 6

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Forsythia x intermedia

&lt;400&gt; 6

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Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu  
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Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu  
 35 40 45

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Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr  
 50 55 60  
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp  
 65 70 75 80  
 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala  
 85 90 95  
 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala  
 100 105 110  
 Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe  
 115 120 125  
 Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile  
 130 135 140  
 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His  
 145 150 155 160  
 Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu  
 165 170 175  
 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro  
 180 185 190  
 Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn  
 195 200 205  
 Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly  
 210 215 220  
 Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala  
 225 230 235 240  
 Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly  
 245 250 255  
 Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp  
 260 265 270

Ser

<210> 7  
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 <213> Forsythia x intermedia

<220>  
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gga aaa gtt gcc ctt ata aca gga gga gcc agt gga att gga gaa ttc				96
Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Phe	20	25	30	
aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat				144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp	35	40	45	
gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc atc ggc act tcc				192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser	50	55	60	
aat tcc atc tac atc cac tgc gat gtt acc aat gaa gac gat gtt aaa				240
Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys	65	70	75	80
aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg				288
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met	85	90	95	
ttc aac aat gca gga att gct gac ccc aac aag ccc cgc atc gta gac				336
Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp	100	105	110	
aac gaa aaa gca gac ttt gaa cgc gtt ctc agc gta aat gta acc ggt				384
Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly	115	120	125	
gtt ttc cta tgc atg aag cac gca gca cgc gtt atg gtg cca gca cgc				432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg	130	135	140	
agt ggc agc ata att tcc act gct agc gta agc tca aca att ggt ggt				480
Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly	145	150	155	160
gct gct tca cat gct tat tgt tgt tca aag cat gct gtg tta ggc ctt				528
Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu	165	170	175	
act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat				576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn	180	185	190	
tgt ttg gct cct tac gcg ctt gct acg cct tta gcc aag aaa ttt gta				624
Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val	195	200	205	
ggg ctt gaa aat gac gaa gat ttg gag aat gca atg agc ctt atg gga				672
Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly	210	215	220	
aat ctg aaa ggt aca aat ttg aag gct gag gac gtc gcc aat gca gct				720
Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala	225	230	235	240

-10-

ctt tat ctg gca agt gat gag gca aaa tat gtg agt gga cac aat ctg 768  
 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu  
 245 250 255  
 ttc att gat gga ggg ttc agc gtc tac aat tct gca atc aaa atg ttc 816  
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 260 265 270  
 caa tat cca gac act 831  
 Gln Tyr Pro Asp Thr  
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 Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp  
 35 40 45  
 Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser  
 50 55 60  
 Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys  
 65 70 75 80  
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 85 90 95  
 Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp  
 100 105 110  
 Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly  
 115 120 125  
 Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg  
 130 135 140  
 Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly  
 145 150 155 160  
 Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu  
 165 170 175  
 Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn  
 180 185 190  
 Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val  
 195 200 205

-11-

Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly  
 210 215 220

Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala  
 225 230 235 240

Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu  
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Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Ala Ile Lys Met Phe  
 260 265 270

Gln Tyr Pro Asp Thr  
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aaa gtt gcc ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca 96  
 Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr  
 20 25 30

gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc 144  
 Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val  
 35 40 45

caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc ctt tcc aat 192  
 Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn  
 50 55 60

tcc acc tac atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat 240  
 Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn  
 65 70 75 80

gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg ttc 288  
 Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe  
 85 90 95

aac aat gca gga att tct gat ccc tac aag ccc cgg gtc ata gac aac 336  
 Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn  
 100 105 110

gaa aaa gca gac ttt gaa cgc gtt ctc agt gtt aat gta acc gga gtt 384  
 Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val  
 115 120 125

ttc cta ttt atg aag cac gca gca cgc att atg gtt cca gca cga agt 432  
 Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser  
 130 135 140  
 ggc tgc ata att tcc act gct agt tta agc tca act atg ggt ggt ggt 480  
 Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly  
 145 150 155 160  
 tct tca cat gct tat tgt ggt tca aag cat gct gta tta ggc ctt act 528  
 Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr  
 165 170 175  
 agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt 576  
 Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys  
 180 185 190  
 ttg tct cct ttc ggg ctt cct acg cct tta gcc aag aaa ttt aca ggg 624  
 Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly  
 195 200 205  
 att gaa aat gat gaa gac ttg gcg aat gga ata gaa cgt gcg gga aat 672  
 Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn  
 210 215 220  
 ctg aaa ggt aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt 720  
 Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu  
 225 230 235 240  
 ttt ctg gct agt gat gag gca caa tat gtg agt gga caa aat ctg ttc 768  
 Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe  
 245 250 255  
 atc gat gga ggg ttc agc gtc tgc aat tct gca atc aaa ttg ttc caa 816  
 Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln  
 260 265 270  
 tat cca gac tct 828  
 Tyr Pro Asp Ser  
 275

&lt;210&gt; 10

&lt;211&gt; 276

&lt;212&gt; PRT

&lt;213&gt; Forsythia x intermedia

&lt;400&gt; 10

Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly  
 1 5 10 15

Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr  
 20 25 30

Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val  
 35 40 45

Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn  
 50 55 60

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Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn  
 65 70 75 80  
 Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe  
 85 90 95  
 Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn  
 100 105 110  
 Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val  
 115 120 125  
 Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser  
 130 135 140  
 Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly  
 145 150 155 160  
 Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr  
 165 170 175  
 Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys  
 180 185 190  
 Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly  
 195 200 205  
 Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn  
 210 215 220  
 Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu  
 225 230 235 240  
 Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe  
 245 250 255  
 Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln  
 260 265 270  
 Tyr Pro Asp Ser  
 275

<210> 11  
 <211> 21  
 <212> PRT  
 <213> Forsythia x intermedia

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> N-terminal peptide of F. intermedia  
 secoisolariciresinol protein wherein Xaa at  
 positions 3, 12 and 20 represents an unidentified  
 amino acid residue

<400> 11

-14-

Gln Val Xaa Thr Ala Ile Ala Arg Asp Leu Glu Xaa Lys Val Ala Leu  
 1 5 10 15

Ile Thr Gly Xaa Ala  
 20

<210> 12  
 <211> 17  
 <212> PRT  
 <213> Forsythia x intermedia

<400> 12  
 Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala  
 1 5 10 15

Lys

<210> 13  
 <211> 15  
 <212> PRT  
 <213> Forsythia x intermedia

<400> 13  
 Leu Asn Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Lys  
 1 5 10 15

<210> 14  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide

<220>  
 <221> misc\_feature  
 <222> (1)..(20)  
 <223> PCR primer wherein n at positions 3, 9, 15 and 18  
 represents inosine

<400> 14  
 ggnathggng aracnacngc

20

<210> 15  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> PCR primer wherein n at positions 3 and 9  
represents inosine

<400> 15  
ccngcrttng araacatdat

20

<210> 16  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> PCR primer wherein n at positions 3 and 9  
represents inosine

<400> 16  
ccngcrttnc traacatdat

20

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> PCR primer

<400> 17  
attccgctag attgcattga

20

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature

<222> (1)..(20)  
<223> PCR primer wherein n at positions 3 and 9  
represent inosine

<400> 18  
ccngcrttnc traacatdat

20

<210> 19  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(20)  
<223> T7 PCR primer

<400> 19  
aattaaccct cactaaaggg

20

<210> 20  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(23)  
<223> PCR primer

<400> 20  
cagcttcgaa ctgcattcgc aag

23

<210> 21  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<220>  
<221> misc\_feature  
<222> (1)..(22)  
<223> T7 PCR primer



<400> 21  
cgggatatca ctcagcataa tg

22

<210> 22  
<211> 816  
<212> DNA  
<213> Forsythia x intermedia

<220>  
<221> CDS  
<222> (1)..(816)

<400> 22  
cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc ctt 48  
Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu  
1 5 10 15  
ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc ttc 96  
Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe  
20 25 30  
tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa tta 144  
Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu  
35 40 45  
ggg cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac atc 192  
Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile  
50 55 60  
cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac aac 240  
His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn  
65 70 75 80  
aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca gga 288  
Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly  
85 90 95  
att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca gac 336  
Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp  
100 105 110  
ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc atg 384  
Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met  
115 120 125  
aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata att 432  
Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile  
130 135 140  
tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat gcc 480  
Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala  
145 150 155 160  
tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg gca 528  
Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala  
165 170 175

gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct ttc 576  
 Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe  
 180 185 190

ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat gaa 624  
 Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu  
 195 200 205

gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt cca 672  
 Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro  
 210 215 220

aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct agt 720  
 Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser  
 225 230 235 240

gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga ggg 768  
 Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly  
 245 250 255

ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat tct 816  
 Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser  
 260 265 270

&lt;210&gt; 23

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Forsythia x intermedia

&lt;400&gt; 23

Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu  
 1 5 10 15

Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe  
 20 25 30

Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu  
 35 40 45

Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile  
 50 55 60

His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn  
 65 70 75 80

Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly  
 85 90 95

Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp  
 100 105 110

Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met  
 115 120 125

Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile  
 130 135 140

Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala  
 145 150 155 160  
 Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala  
 165 170 175  
 Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe  
 180 185 190  
 Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu  
 195 200 205  
 Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro  
 210 215 220  
 Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser  
 225 230 235 240  
 Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly  
 245 250 255  
 Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser  
 260 265 270

<210> 24  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide

<220>  
 <221> misc\_feature  
 <222> (1)..(33)  
 <223> PCR primer

<400> 24  
 acatatgcag cttcgaaactg cattcgcaag aag

33

<210> 25  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide

<220>  
 <221> misc\_feature  
 <222> (1)..(33)  
 <223> PCR primer

<400> 25

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catatgggca gacatgttac atgatcaatt gca

33